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James Martinell  
Primary Examiner 1634

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60358 STRANDED/BI 46640 STRANDED/AB  
88738 LIBRAR?/BI 80372 LIBRAR?/AB  
99221 CIRCULAR?/BI 74733 CIRCULAR?/AB  
L1 5  
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DALL ----- ALL, delimited (end of each field identified)  
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FBIB ----- AN, BIB, plus Patent FAM  
IND ----- Indexing data  
IPC ----- International Patent Classifications  
MAX ----- ALL, plus Patent FAM, RE  
PATS ----- PI, SO  
SAM ----- CC, SX, TI, ST, IT  
SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers; SCAN must be entered on the same line as the DISPLAY, e.g., D SCAN or DISPLAY SCAN)  
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IALI ----- ALL, indented with text labels  
IBIB ----- BIB, indented with text labels  
IMAX ----- MAX, indented with text labels  
ISTD ----- STD, indented with text labels

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HITSTR ----- HIT RN, its text modification, its CA index name, and its structure diagram  
HITSEQ ----- HIT RN, its text modification, its CA index name, its structure diagram, plus NTE and SEQ fields  
FHITSTR ----- First HIT RN, its text modification, its CA index name, and its structure diagram  
FHITSEQ ----- First HIT RN, its text modification, its CA index name, its structure diagram, plus NTE and SEQ fields  
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BIB ----- AN, plus Bibliographic Data and PI table (default)  
CAN ----- List of CA abstract numbers without answer numbers  
CBIB ----- AN, plus Compressed Bibliographic Data  
CLASS ----- IPC, NCL, ECLA, FTERM  
DALL ----- ALL, delimited (end of each field identified)  
DMAX ----- MAX, delimited for post-processing  
FAM ----- AN, PI and PRAI in table, plus Patent Family data  
FBIB ----- AN, BIB, plus Patent FAM  
IND ----- Indexing data  
IPC ----- International Patent Classifications  
MAX ----- ALL, plus Patent FAM, RE  
PATs ----- PI, SO  
SAM ----- CC, SX, TI, ST, IT

SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers; SCAN must be entered on the same line as the DISPLAY, e.g., D SCAN or DISPLAY SCAN)  
STD ----- BIB, CLASS

IABS ----- ABS, indented with text labels  
IALI ----- ALL, indented with text labels  
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IMAX ----- MAX, indented with text labels  
ISTD ----- STD, indented with text labels

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SIBIB ----- IBIB, no citations

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ENTER DISPLAY FORMAT (BIB):bib

L1 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 2004:759719 CAPLUS  
DN 141:272586  
TI Method of constructing a circular DNA library by partial homologous recombination of DNA chain  
IN Kondo, Kazuhiro; Oishi, Michio; Ohara, Osamu  
PA Aisin Cosmos R & D Co., Ltd., USA; Kazusa DNA Research Institute Foundation  
SO U.S. Pat. Appl. Publ., 17 pp. CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION  
NO. DATE -----

PI US 2004180374 A1 20040916 US 2004-798750  
20040310 JP 2004275032 A2 20041007 JP 2003-68176  
20030313  
PRAI JP 2003-68176 A 20030313

L1 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 2002:632407 CAPLUS  
DN 138:67428  
TI Identification of novel bovine RPE and retinal genes by  
subtractive hybridization  
AU Sharma, Shiwani; Chang, Jinghua T.; Della, Neil G.;  
Campochiaro, Peter A.; Zack, Donald J.  
CS Department of Ophthalmology, Flinders University, Bedford  
Park, South Australia, Australia  
SO Molecular Vision [online computer file] (2002), 8, 251-258  
CODEN: MVEPFB; ISSN: 1090-0535 URL:  
<http://www.molvis.org/molvis/v8/a32/sharma.pdf>  
PB Molecular Vision  
DT Journal; (online computer file)  
LA English  
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE  
FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE  
FORMAT

L1 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 1998:15658 CAPLUS  
DN 128:98540  
TI Procedure for normalization of cDNA libraries  
IN Bonaldo, Maria Defatima; Soares, Marcelo Bento  
PA Trustees of Columbia University In the City of New York,  
USA  
SO U.S., 8 pp. CODEN: USXXAM  
DT Patent  
LA English  
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION  
NO. DATE -----  
-----  
PI US 5702898 A 19971230 US 1995-465857  
19950606  
PRAI US 1995-465857 19950606

L1 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 1992:249647 CAPLUS  
DN 116:249647  
TI Construction of small-insert genomic DNA libraries highly  
enriched for microsatellite repeat sequences  
AU Ostrander, Elaine A.; Jong, Pam M.; Rine, Jasper; Duyk,  
Geoffrey  
CS Dep. Mol. Cell. Biol., Univ. California, Berkeley, CA, 94720,  
USA  
SO Proceedings of the National Academy of Sciences of the  
United States of America (1992), 89(8), 3419-23 CODEN:  
PNASA6; ISSN: 0027-8424  
DT Journal  
LA English

L1 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 1991:443429 CAPLUS  
DN 115:43429  
TI A simple and efficient cDNA library subtraction procedure:  
isolation of human retina-specific cDNA clones  
AU Swaroop, Anand; Xu, Junzhe; Agarwal, Neeraj; Weissman,  
Sherman M.  
CS Kellogg Eye Cent., Univ. Michigan, Ann Arbor, MI, 48105,  
USA

SO Nucleic Acids Research (1991), 19(8), 1954 CODEN:  
NARHAD; ISSN: 0305-1048  
DT Journal  
LA English

=> d l1 1-5 bib ab

L1 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 2004:759719 CAPLUS  
DN 141:272586  
TI Method of constructing a circular DNA library by partial  
homologous recombination of DNA chain  
IN Kondo, Kazuhiro; Oishi, Michio; Ohara, Osamu  
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Institute Foundation  
SO U.S. Pat. Appl. Publ., 17 pp. CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION  
NO. DATE -----  
-----  
PI US 2004180374 A1 20040916 US 2004-798750  
20040310 JP 2004275032 A2 20041007 JP 2003-68176  
20030313  
PRAI JP 2003-68176 A 20030313  
AB The present invention provides a method of constructing a  
circular DNA library having an increased content of a desired  
nucleic acid by removing a specific DNA from the circular DNA  
library by using a RecA protein. More specifically, the present  
invention provides a method of constructing a DNA library having  
an increased content of the first dsDNA by removing a second  
dsDNA different from the first dsDNA from a DNA library contg.  
the first dsDNA to be increased in content and the second  
dsDNA.

L1 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 2002:632407 CAPLUS  
DN 138:67428  
TI Identification of novel bovine RPE and retinal genes by  
subtractive hybridization  
AU Sharma, Shiwani; Chang, Jinghua T.; Della, Neil G.;  
Campochiaro, Peter A.; Zack, Donald J.  
CS Department of Ophthalmology, Flinders University, Bedford  
Park, South Australia, Australia  
SO Molecular Vision [online computer file] (2002), 8, 251-258  
CODEN: MVEPFB; ISSN: 1090-0535 URL:  
<http://www.molvis.org/molvis/v8/a32/sharma.pdf>  
PB Molecular Vision  
DT Journal; (online computer file)  
LA English  
AB Purpose: Understanding of the specialized function of the  
retinal pigment epithelium (RPE) can be aided by the  
identification and characterization of genes that are preferentially  
expressed in the RPE. With this aim, the authors undertook a  
systematic effort to identify and begin characterization of such  
genes. Methods: A subtracted bovine RPE cDNA library was  
generated through subtractive hybridization using a  
\*\*\*single\*\*\* - \*\*\*stranded\*\*\* \*\*\*circular\*\*\* bovine RPE  
cDNA \*\*\*library\*\*\* as target and biotinylated mRNA from  
bovine heart and liver as alternate drivers. Approx. one thousand  
of the resulting subtracted cDNA clones were partially sequenced  
and analyzed, and a non-redundant set of one hundred of these  
cDNAs were examd. for tissue expression pattern using a mini-  
Northern blot procedure and for identity by sequence anal.  
Results: The subtraction method successfully allowed the

enrichment of cDNAs that are preferentially expressed in the RPE. Out of the analyzed clones, expression of forty-five clones was verifiable by Northern blotting. Of these, a significant proportion of cDNAs were preferentially expressed in the RPE. The authors obsd. that the expression of some subtracted cDNAs was restricted to the retina and no expression was detected in the RPE. These retinal clones were obtained in addn. to RPE clones presumably because the initial RPE RNA population was contaminated with a small proportion of retinal RNA. Two thirds of the identified RPE and retinal cDNAs are likely to represent novel genes because they do not have homol. to known genes in the databases. Conclusions: Genes that are specifically or predominantly expressed in the RPE/retina are likely to be important for retinal function. The authors have identified novel cDNAs from bovine RPE and retina by subtractive hybridization. These cDNAs can be used as starting material for the identification of corresponding human genes expressed in the RPE and retina. The human genes thus identified are likely to contain good candidate genes for retinal disease.

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L1 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN  
AN 1998:15658 CAPLUS

DN 128:98540

TI Procedure for normalization of cDNA libraries

IN Bonaldo, Maria Defatima; Soares, Marcelo Bento

PA Trustees of Columbia University In the City of New York, USA

SO U.S., 8 pp. CODEN: USXXAM

DT Patent

LA English

FAN.CNT 1 PATENT NO.	KIND	DATE	APPLICATION
NO. DATE	----	-----	-----

PI US 5702898 A 19971230 US 1995-465857  
19950606

PRAI US 1995-465857 19950606

AB This invention provides a method to normalize a cDNA library constructed in a vector capable of being converted to single-stranded circles and capable of producing complementary nucleic acid mols. to the single-stranded circles comprising: (a) converting the cDNA library in single-stranded circles; (b) generating complementary nucleic acid mols. to the single-stranded circles; (c) hybridizing the single-stranded circles converted in step (a) with complementary nucleic acid mols. of step (b) to produce partial duplexes to an appropriate Cot; (e) sepg. the unhybridized single-stranded circles from the hybridized single-stranded circles, thereby generating a normalized cDNA library. The procedure has several advantages. First of all, because an excess of complementary nucleic acid mols. (antisense RNA) is used, there is no competition between full-length and truncated versions for complementary fragments and therefore there is no bias against longer clones. Second, since the synthesis is driven by an RNA promoter, even those clones without tail will be represented in the normalized library. Third, since the driver concn. is high, a Cot of 5-50 can be achieved in a few hours of incubation, thus making the procedure much quicker. Finally, only one step of hydroxylapatite purifn. is required, thus making the procedure considerably simpler and quicker. The procedure was applied to cDNA libraries from human placenta, breast tissue, pineal gland, retina, and ovarian tumor.

L1 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

AN 1992:249647 CAPLUS

DN 116:249647

TI Construction of small-insert genomic DNA libraries highly enriched for microsatellite repeat sequences

AU Ostrander, Elaine A.; Jong, Pam M.; Rine, Jasper; Duyk, Geoffrey

CS Dep. Mol. Cell. Biol., Univ. California, Berkeley, CA, 94720, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1992), 89(8), 3419-23 CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB An efficient method for the construction of small-insert genomic libraries enriched for highly polymorphic, simple sequence repeats is described. With this approach, libraries in which 40-50% of the members contain (CA)<sub>n</sub> repeats are produced, representing an .apprxq.50-fold enrichment over conventional small-insert genomic DNA libraries. Briefly, a genomic library with an av. insert size of <500 base pairs was constructed in a phagemid vector. Amplification of this library in a dut ung strain of Escherichia coli allowed the recovery of the \*\*\*library\*\*\* as closed \*\*\*circular\*\*\* \*\*\*single\*\*\* - \*\*\*stranded\*\*\* DNA with uracil frequently incorporated in place of thymine. This DNA was used as a template for second-strand DNA synthesis, primed with (CA)<sub>n</sub> or (TG)<sub>n</sub> oligonucleotides, at elevated temps. by a thermostable DNA polymerase. Transformation of this mixt. into wild-type E. coli strains resulted in the recovery of primer-extended products as a consequence of the strong genetic selection against single-stranded uracil-contg. DNA mols. In this manner, a library highly enriched for the targeted microsatellite-contg. clones was recovered. This approach is widely applicable and can be used to generate marker-selected libraries bearing any simple sequence repeat from cDNAs, whole genomes, single chromosomes, or more restricted chromosomal regions of interest.

L1 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

AN 1991:443429 CAPLUS

DN 115:43429

TI A simple and efficient cDNA library subtraction procedure: isolation of human retina-specific cDNA clones

AU Swaroop, Anand; Xu, Junzhe; Agarwal, Neeraj; Weissman, Sherman M.

CS Kellogg Eye Cent., Univ. Michigan, Ann Arbor, MI, 48105, USA

SO Nucleic Acids Research (1991), 19(8), 1954 CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB A biotin-based subtraction procedure was used to enrich human adult retina cDNA library for specific clones. The directional cDNA libraries from the human adult retina and JY lymphoblastoid cell line were constructed in Charon BS (-) vector and were then transferred to plasmid BS (-). The plasmid retina cDNA \*\*\*library\*\*\* was used to generate \*\*\*single\*\*\* \*\*\*stranded\*\*\* (ss) \*\*\*circular\*\*\* DNA with helper phage R408 (Stratagene protocol). The double stranded plasmid DNA from JY cDNA library was used to synthesize biotinylated run off transcripts with Bio-11-UTP. Since the two cDNA libraries have directional cDNA inserts, T3 RNA polymerase would generate JY biotinylated RNA that is complementary to the orientation of cDNAs in retina ss DNA species, ss DNA from retina library was annealed to biotinylated RNA from JY library in a sealed capillary. After hybridization, the mixt. was incubated with 250 mg vectrex-avidin. The ss DNA in the unbound fraction (enriched for retina

specific ss DNA) was pptd. in the presence of glycogen, and an aliquot of it was used directly to electrotransform XL1 blue cells (Bio-Rad Gene Pulser/Pulse Controller). Between 2-15% of the clones are recovered after subtraction. The ratio of blue vs. white colonies is increased dramatically in the subtracted library because of the simultaneous enrichment of non-insert contg. ss DNA mols. Forty randomly picked white colonies from 2 subtracted retina libraries were characterized by Southern anal. of DNA from cDNA libraries, and/or by Northern anal. of total RNA. Almost 70% of the clones are not detectable in the JY cDNA library against which the retina library was subtracted, and this included several novel retina-specific cDNAs. Similar results were obtained with the anal. of 15 cDNA clones from a subtracted retinal pigment epithelium library. The complementarity of the hybridizing species from two directional cDNA libraries, use of RNA polymerase to obtain large amounts of biotinylated driver RNA and direct transformation of ss DNA obtained in the unbound fraction further improves the efficiency of the subtraction procedure.

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L1 5 S

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L2	81	((single adj stranded) near5 librar\$) near5 circular\$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/14 14:27
L3	1137784	@rlad<"20030725"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/14 14:27
L4	58	l2 and l3	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/14 14:27